SEQUENCE LISTING

<110> University of Utah Research Foundation

    Bock, Susan C.

<120> Methods of Using High Affinity ATIII
   Variants

<130> 21101.0054P1

<150> 60/618,746
<151> 2004-10-14

<150> 60/535,360
<151> 2004-01-09

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
    Synthetic Construct

<400> 1
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Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
 1               5                  10                  15
Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
            20                  25                  30
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
            35                  40                  45
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
    50                  55                  60
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
65                  70                  75                  80
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
            85                  90                  95
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
            100                 105                 110
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
            115                 120                 125
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
    130                 135                 140
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
145                 150                 155                 160
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
            165                 170                 175
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
            180                 185                 190
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
            195                 200                 205
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
    210                 215                 220
```

```
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
225                     230                 235                 240
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
                245                 250                 255
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
            260                 265                 270
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
        275                 280                 285
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
    290                 295                 300
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
305                 310                 315                 320
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
            325                 330                 335
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
            340                 345                 350
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
            355                 360                 365
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
370                 375                 380
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
385                 390                 395                 400
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
            405                 410                 415
Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
            420                 425                 430
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
            435                 440                 445
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
    450                 455                 460
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<210> 2

<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      Synthetic Construct

<400> 2
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atgtattcca atgtgatagg aactgtaacc tctggaaaaa ggaaggttta tcttttgtcc     180
ttgctgctca ttggcttctg ggactgcgtg acctgtcacg ggagccctgt ggacatctgc     240
acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag     300
aaggcaactg aggatgaggg ctcagaacag aagatcccgg aggccaccaa ccggcgtgtc     360
tgggaactgt ccaaggccaa ttcccgcttt gctaccactt ctatcagca cctggcagat     420
tccaagaatg acaatgataa cattttcctg tcacccctga gtatctccac ggcttttgct     480
atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt     540
gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc     600
cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg ccttttttgga     660
gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttggt atatggagcc     720
aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa     780
tgggtgtcca ataagaccga aggccgaatc accgatgtca ttccctcgga agccatcaat     840
gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag     900
ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca     960
gcatctatga gtgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcacccag    1020
gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct    1080
gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg    1140
```

```
gatgaattgg aggagatgat gctggtggtt cacatgcccc gcttccgcat tgaggacggc        1200
ttcagtttga aggagcagct gcaagacatg ggccttgtcg atctgttcag ccctgaaaag        1260
tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc        1320
cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt        1380
gtgattgctg gccgttcgct aaaccccaac agggtgactt tcaaggccaa caggcccttc        1440
ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac        1500
ccttgtgtta agtaaaatgt tcttattctt tgcacctctt cctatttttg gtttgtgaac        1560
agaagtaaaa ataaatacaa actacttcca tctcacatt                              1599
```